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Result
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                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Query
Score Match Length DB
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1: gb_ba1:*
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## ALIGNMENTS

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source	FEATURES		JOURNAL	TITLE	AUTHORS	REFERENCE	JOURNAL		TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	NID	ACCESSION	DEFINITION	LOCUS	AF035528	RESULT 1
12887	Location/Qualifiers	Rockefeller University, 1230 York Avenue, New York, NY 10021, USA	Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The	Direct Submission	Hata, A., Lagna, G., Massague, J. and Hemmati-Brivanlou, A.	2 (bases 1 to 2887)	Genes Dev. (1997) In press	the Smad4 tumor suppressor	Smad6 inhibits BMP/Smad1 signaling by specifically competing with	Hata, A., Lagna, G., Massague, J. and Hemmati-Brivanlou, A.	1 (bases 1 to 2887)	Primates; Catarrhini; Hominidae; Homo.	Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	Homo sapiens	human.	•	g2736315	AF035528	Homo sapiens Smad6 mRNA, complete cds.	AF035528 2887 bp mRNA PRI 01-JAN-1998		

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/db_xref="piD:g2736316"
/translation="MFRSKRSGLVRRLMRSRVVPNREEGGSGGGGDEDGSLGSRAE
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ARSRLLLEOELKTVTYSLLKRLKERSLDTLLEAVESRGVPGGCVLVPRADLRLGQ
PAPPOLLLGRLFRWPDLOHAVESDSTLSVTETEATNSLLTAPGSFSDASMSPDATKPSHMCSV
AYWEHRTRVGRLYAVYDQAVSIFYDLPQGSGFCLGQLMLGRSESVRRTERSKIGFGIL
LSKEEDGVMAYNRGEHPJFVNGSPTLANGGRALVVRKVPPGYSIKVFDFERSGLOHAP
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/db_xref="taxon:9606"
/cell_line="Jurkat T-cell"
937. .2427
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Best Local Similarity
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                                                                                                                                                                CCCCCACCCCTGGCGCCAAAGGATATTGTATGTTCAGGTCCAAAACGCTCGGGGCCTGGTGC 967
                                                                               GGCGACTTTGGCGAAGTCGTGTGGTCCCCAACCGGGAGGAAGGCGGCAGCGGCGGCGGCGGCG 1027
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AF035528
g2736315
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Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The Submitted (21-NOV-1997) Laboratory of Molecular Embryology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA Location/Qualifiers
1. 2887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 2887)
Hata,A., Lagna,G., Massague,J. and Hemmati-Brivanlou,A.
Smad6 inhibits BMP/Smad1 signaling by specifically competing with
the Smad4 tumor suppressor
Genes Dev. (1997) In press
2 (bases 1 to 2887)
Hata,A., Lagna,G., Massague,J. and Hemmati-Brivanlou,A.
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937. .2427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="inhibitor of BMP signaling"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Smad6"
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O; Mismatches 15;
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TCCTGCTCAGCAAGGAGCCCGACGGCGTGTGGGCCTACAACCGCGGCGAGCACCCCATCT 1385	7 1326 5 2108	Db Qy
TCAACCTGGAGCAGCGCAGCGAGTCGGTGCGGCGAACGCGCAGCAAGATCGGCTTCGGCA 1325	1266	p So
ACCAGGCCGTCAGCATCTTCTACGACCTACCTCAGGGCAGCGGCTTCTGCCTGGGCCAGC 1265		g dq Qy
TGCAGCGTGGCGTACTGGGAGCACCGGACGCGCGTGGGCCGCCTCTATGCGGTGTACG 120 	114	d do
CTGCTCCGGGTGAATTCTCAGACGCCAGCATGTCTCCGGACGCCACCAACGAGGCCAGCCA	1086	g dy
TGGATCTGTCCGATTCCACATTGTCTTACACTGAAACGGAGGCTACCAACTCCCTCATCA 1085	1026	Db Qy
GGCCCGAATCTCCGCCACCTCCCTACTCTCGGCTGTCTCCTCGCGACGAGTACAAGCCAC 1025	966 1748	pb Qy
CCGCCGCCGACGGCCTACCGTGTGCTGCAACCCCTACCACTTCAGCCGGCTCTGCG 965	906 1688	Db Db
GCTGGCCCGACCTGCAGCACGCCGTGGAGCTGAAGCCCCTGTGCGGCTGCCACAGCTTCG 905	7 846 5 1628	Db Qy
CCGACCTCCGCCTGGGCGGCCAGCCCGCGCGCGCGCGCGC	7 786 5 1568	Db Qy
TGCTGGAGGCGGTGGAGTCCCGCGGCGGCGGCTGCCGGCTGCGTGCTGGTGCCGCGCG 785	7 726 5 1508	DE QY
AACTCAAAACCGTCACGTACTCGCTGCTGAAGCGGCTCAAGGAGCGCTCGCT	0 1448	D Qy
AGCCGGCGGCGGCGGAGTCGCGAAGCGCGCTCGCGGCTGCTGCTGCTGCAGCAGG 665	606	dg Qy
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GAGGCCCGGGCTGCCTGCCCGAGAGTGACTGCGAGACGGTGACCTGCTGTCTTTTCGG 545	7 486 5 1268	dd Qy
GGCCCATGTCGGAGCCAGGGGCCGGCGCTGGGAGCTCCCTGCTGGACGTGGCGGAGCCGG 485	426 5 1208	Db Qy
CAGTGGGACAGCGAGGCGCCCAGGGCGCGGGGAGGCGCCGGCGCGCAGGGGGCCCCCC	7 366 5 1148	Dt. Qy
AGGGCGGAGGCTGCGGCCCCCGAAGTCCGCCCGGTAGCCCCGGGGCGCCCCGGGACG 365	7 306 5 1088	Db Qy

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BASE
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Homo sapiens
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(bases 1 to 1491)
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                                                                                                                                                                                                                                                                                                     human
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EPDAADGPYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILLNNPR"
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Uppsala 751 24, Sweden
                                                                                                                                                                                                                                             Submission
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Query Match
Best Local Similarity
Matches 1491; Conserv
                    ACTGAAACGGAGGCTACCAACTCCCTCATCACTGCTCCGGGTGAATTCTCAGACGCCAGC
                                                 CGGCTGTCTCCTCGCGACGAGTACAAGCCACTGGATCTGTCCGATTCCACATTGTCTTAC
ATGTCTCCGGACGCCAACCCAAGCCGAGCCACTGGTGCAGCGTGGCGTACTGGGAGCACCGG
                                                                               TGCAACCCCTACCACTTCAGCCGGCTCTGCGGGGCCCGAATCTCCGCCACCTCCCTACTCT
                                                                                                            CCGCCGCAGCTGCTGCTCGGCCGCCTCTTTCGCTGGCCCGAGCTTGCAGCACCGCGTGGAG
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Pred. No. 3.1e-188;
0; Mismatches 0;
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Primates; Catarrhini; Hominidae; Homo.
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Drive, Bethesda, MD 20892, USA
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                                                                                                                                                                            Direct Submission
Submitted (23-JUN-1997) Biochemistry, The
Tokyo, 1-37-1 Kami-Tkebukuro, Toshima-ku,
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Smad6 inhibits signalling by the TGF-beta superfamily
Nature 389 (6651), 622-626 (1997)
97474481
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Mus musculus
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                                                                                                                                                                                                                                                                     (bases 1 to 1488)
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                                                                                             /db_xref="taxon:10090"
1. .1488
                                                                                                                             /organism="Mus musculus
                                                                             'gene="mSmad6"
                                                                                                                                                                    Location/Qualifiers
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-ku, Tokyo 170, Japan
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BASE COUNT
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/db_xref="PID:g2507640"
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PLDVAEPGGPGMLPESDCETYTCCLFSERDAAGAPRDSSUDPQARGSPEREEGGGPRSR
PLDVAEPGGPMLPESDCETYTGLLKRLKERSLDTLLEAVESRGGVPGGCVLVPRADLRLGG
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PLSWEHRTRVGRLYAVYDQAVSLFYDLPGGSGFCLGQLNLEGRSESVRRTRSKIGEGI
LLSKEPDGVWAYURGEHPIFVNSPTLDAPGGRALVVRKVPBGYSKYPDFERSGLLQH
ADAAHGSYDPHSVRLISFAKGWGPCYSROFITSCPCWLEILLNNHR"
235 a 505 c 505 g 242 t 1 others
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Query Match
Best Local Similarity
Matches 1355; Conserv
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                                                                               CTGCTCAAGAGGCTCAAGGAGCGTTCGCTGGACACGCTGTTGGAGGCTGTGGAGTCCCGA
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source
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1 (bases 1 to 1280)

Riggins,G.J., Thiagalingam,S., Rozenblum Kern,S.E., Hamilton,S.R., Willson,J.K., Kinzler,K.W. and Vogelstein,B. Mad-related genes in the human Mad-related genes in the human
                                                                                                                                                                                                         Human
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                                                                                                                                                  Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; F
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        Submitted (04-JUN-1996) Oncology Center, Rm. 1
424 N. Bond St., Baltimore, MD 21231, USA
On NOV 1, 1996 this sequence version replaced
Location/Qualifiers
1, 1280
                                                                                                                                                                               human
                                                               Riggins, G
                                                        Direct Submission
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chromosome 1
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/organism="Homo sapiens
                                                              Thiagalingam, S., Kinzler, K.W.
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                                                                   Vogelstein, B.V.
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              CCGTCAGCATCTTCTACGACCTACCTCAGGGCAGCGGCTTCTGCCTGGGCCAGCTCAACC
                                                 GCGTGGCGTACTGGGAGCACCGGACGCGCGTGGGGCCGCCTCTATGCGGTGTACGACCAGG
                                                                                             CGGGTGAATTCTCAGACGCCAGCATGTCTCCGGACGCCACCAAGCCGAGCCACTGGTGCA 1151
                                                                 GCGTGGCGTACTGGGAGCACCGGACGCGCGTGGGGCCGCCTCTATGCGGTGTACGACCAGG
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Riggins,G.J., Thiagalingam,S., Rozenblum,E., Weinstein,C Kern,S.E., Hamilton,S.R., Willson,J.K., Markowitz,S.D., Kinzler,K.W. and Vogelstein,B.
Mad-related genes in the human Nature Genet. 13 (3), 347-349 (1996)
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Riggins,G.J., Thiaga
Direct Submission
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GRALVVRKVPPGYSIKVFDFERSGLQHAPEPDAADGPYDPNSVRISFAKGWGPCYSRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Mad homolog"
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99.3%;
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Pred. No. 1.6e-101;
0; Mismatches 6;
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                                                             2 (bases 1 to 2051)
Nakayama,T., Gardner,H. and Christian,J.L.
Direct Submission
Submitted (07-JAN-1998) Department of Cell and Developmental
Biology, Oregon Health Sciences University, 3181 SW Sam Jacks
Park Road, Portland, OR 97201-3098, USA
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/db_xref="taxon:8355"
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/gene="Smad6"
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                   CAGACGCCAGCATGTCTCCGGACGCCACCAAGCCGAGCCACTGGTGCAGCGTGGCGTACT 1163
                                                                                        CATTGTCTTACACTGAAACGGAGGCTACCAACTCCCTCATCACTGCTCCGGGTGAATTCT
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/note="inhibitory Mad-related protein"
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Rockefeller University, 1230 York Avenue, New York, NY 10021,
                                                                                                                                                                                                                                                                                                                                           Hata,A., Lagna,G., Massague,J.
Direct Submission
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195
                                            /product="Smad6"
//db_xref="pid:92736318"
//db_xref="pid:92736318"
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//translation="VTRHEGPPHLLLCRLFRWPELQHPGQLKALSGCQGAGGSDNNSG
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TSLSPDMSKQGHWCSVAXWEHRTRVGRLYAVCQPSVSIFYDLPQGSGFCLGQLNLENR
TSLSPDMSKQGHWCSVAXWEHRTRVGRLYAVCQPSVSIFYDLPQGSGFCLGQLNLENR
SEAAARTRGKIGLGIVLSRETDGVWAXNRSDHFIFNBSTLAPAGGAGAT
                             SLKVFDYKKSCVLRHHPTPPEHTDGPYDPNSVRISFAKGWGPCYSRQMITSCPCWLEV
                                                                                                                                             /note="SMAD family member"
/codon_start=1
                                                                                                                                                                                                                          /organism="Xenopus laevis"
/db_xref="taxon:8355"
/tissue_type="head"
                                                                                                                                                                                                         /dev_stage="tadpole"
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                  g3378187
Mad-related protein;
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                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodentia; Sciurognathi; Muridae; Mu (bases 1 to 3681)
Kitamura, K. and Okazaki, K.
Characterization of a novel mouse p
mediate TGF-beta family signalling
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Rodentia; Sciurognathi; Muridae; Murinae;
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                           'LTANS 1 at ion "MFRTKRSALVRRLWRSRAPGGEDEEGVGGGGGGELRGEGATD GRAYGAGGGGAGRAGCCLGKAVRGAKGHHHPHPPTSGAQAGAGAEADLKALTHSVLKK LIKERQLELLLQAVESRGGTRACLLLPGRLDCRLGPGAPASAQPAQPESSYSLPLLLC KVFRWPDLRHSSEVKRLCCCESYGK INPELVCCNEHHLSRLCELESPPPYSRY PMDF LKPTAGGPDAVPSSAETGGTNYLAPGGLSDSQLLLEPGDRSHWCVVAYWEEKTTAVGRL RSYSTIFIKSATLDRDGRGCLGQLNKSQLVQKVYSK IGCGIQLTREVDGVWYYN PTVQLESFYDFYGNGFCLGQLNSDNKSQLVQKVYSK IGCGIQLTREVDGVWYYN FTVQISFVKGRGQCYTRQFISSCPCWLEVIFNSR"
                                                                                                                                                                                       /product="Mad-related protein
/db_xref="PID:e1313653"
/db_xref="PID:93378188"
                                                                                                                                                                                                                                                                                               /gene="smad7"
1437. .2717
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/db_xref="taxon:10090"
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Mus musculus
Eukaryotae; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae; M
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    Nakayama,T.,
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Submitted (21-UUL-1997) Ludwig Institute for Cancer
Uppsala Branch, Box 595, Biomedical Center, Uppsala
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/translation="MERTKRARLVRRLWRSRAPGGEDEEEGVGGGGGGELRGEGATD
/kranslation="MERTKRARLVRRLWRSRAPGGEDEEEGVGGGGGGELRGEGATD
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LKPTAGCPDAVPSSAETGGTNYLAPGGLSDSQLLLEPGDRSHWCYVAYWEEKTRVGRL
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/product="Smad7"
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/db_xref="taxon:10090"
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Pred. No. 3.8e-30
0; Mismatches 54
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Direct Submission
Submitted (30-JUL-1997)
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                                                             Rodentia; Sciurognathi; Muridae; M
1 (bases 1 to 1278)
Kitamura, K. and Okazaki, K.
Isolation of CDNAs encoding mouse
Smad7B) that can mediate TGF-beta
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                                                         Unpublished
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Sciurognathi; Muridae; Murinae;
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       Okazaki
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                                                         homologues of Mad family signalling
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Mad-related protein Smad7B"
//db_xref="PID:e1313655"
//db_xref="PID:e1313655"
//db_xref="PID:e1313655"
//tanslation="MertkrSalvrRlMRSRaPGGEDEEGVGGGGGGELRGEGATD LYCARGGAARAGCCIGKAVRGAKGHHHPHPDTSGACAAGCABADLKALTHSVLKK KYERGLELLLOAVESRGGTRTACLLLPGRLDCRLGPGAPASAOPAQPPSSYSLPLLLC KYPGCPDAVPSSYSLPLLLCLAPGLUCCNPHHLSRLCELESPPPPYSRYPLDC LKPTGCPDAVPSSVETGGTNYLAPGGLSDSQLLLEPGDRSHWCVVAYWEXTRYGRLY SSYPTFIKSATLDNPDSRTLLVHKVEPGFSIKAFDYEKAYSLORPNDHEFMQOPWTNR SSYPTFIKSATLDNPDSRTLLVHKVEPGFSIKAFDYEKAYSLORPNDHEFMQOPWTGF
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382 c
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/note="variation
/citation=[1]
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1. .1278
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/db_xref="taxon:10090"
/dev_stage="17-day embry
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                                             Eukaryotae: Metazoa; Chordata; Vertebrata; Mammalia; primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 3111)

Hayashi, H., Abdollah, S., Qui, Y., Cai, J., Xu, Y.-Y., Grai, Bayashi, H., Abdollah, S., Qui, Y., Gimbrone, M.A., Jr., Wrangichardson, M.A., Topper, J.N., Gimbrone, M.A., Jr., Wrangichardson, M.A., Jr., William, M.A., William, William, M.A., William, M.A., William, M.A., William, M.A., Willi
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                                                                                                                                   Topper,J.N., Cai,J., Qui,Y., Anderson,K.R., Xu,Y.-Y., Deeds,J.D., Feeley,R., Gimeno,C.J., Woolf,E.A., Tayber,O., Mays,G.G., Sampson,B.A., Schoen,F.J., Gimbrone,M.A. Jr. and Falb,D. Vascular MADs: two novel MAD-related genes selectively inducible flow in human vascular endothelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUN-1997) Millennium Drive, Cambridge, MA 02139, USA
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FWYQLSFYKGWGGCYTROFISSCPCWLEVIFNSR"

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/db_xref="taxon:9606"
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                                      ACGGCCCTACGACCCCAACAGCGTCCGCATCAGCTTCGCCAAGGGCTGGGGGCCCTGCT 1580
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Search completed: May 4, 1999, 03:35:35 Job time: 2243 sec



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Apr 30 20:37:57 1999; MasPar time 39.28 Seconds 696.713 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Title:

>US-09-034-286-65 (1-496) from US09034286.pep 3630 1 MFRSKRSGLVRRLWRSRVVP......SRQFITSCPCWLEILLNNPR 496

Scoring table: PAM 150 Gap 11

Searched: 180763 seqs, 55169189 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb18

1:sp\_archea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human 5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle 9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified 13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 48.184; Variance 97.965; scale 0.492

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

20	19	18	17	16	15	14	13	12	11	10	9	æ	7	σ	5	4	ω	2	<b>L</b>	Result
347	347	353	361	361	361	363	515	1219	1239	1242	1242	1245	1293	1315	1508	1646	3349	3627	3630	Score
9.6	9.6	9.7	9.9	9.9	9.9	10.0	14.2	33.6	34.1	34.2	34.2	34.3	35.6	36.2	41.5	45.3	92.3	99.9	100.0	Query Match
425	425	430	467	467	467	467	568	425	426	426	426	425	382		280	235	495	496	496	Length
11	4	4	11	4	11	13	σ	11	11	4	4	11	13	13	13	4	11	4	4	BG
009144	Q92940	014989	Q62432	Q15796	070436	Q91912	015968	088406	035253	014740	015105	088709	057522	057459	057475	Q15799	035182	043541	043654	ij
MOTHERS AGAINST DPP 3	PROTEIN JV15-2 (MAD PR	MOTHER AGAINST DPP (MA	MAD HOMOLOG 2 (MADR2).	JV18-1.	SMAD2 PROTEIN.	MAD2.	DAD POLYPEPTIDE.	SMAD7.	MAD HOMOLOG 8 (SMAD7).	SMAD7 PROTEIN.	MAD-RELATED GENE SMAD7	MAD-RELATED PROTEIN SM	SMAD7.	MAD-RELATED PROTEIN SM	SMAD6 (FRAGMENT).	SMAD6.	MAD HOMOLOG 7 (SMAD6).	SMAD6.	SMAD6.	Description
7.31e-41	7.31e-41	5.63e-42	1.82e-43	1.82e-43	1.82e-43	7.73e-44	7.07e-73	8.70e-215	6.72e-219	1.62e-219	1.62e-219	3.92e-220	5.16e-230	1.51e-234	2.00e-274	4.84e-303	0.00e+00	0.00e+00	0.00e+00	Pred. No.

45	44	43	42	41	40	39	38	37	36	<u>3</u> 5	34	3 3	32	31	30	29	28	27	26	25	24	23	22	21
196	237	237	237	237	262	262	263	310	324	329	329	329	331	331	331	332	329	337	338	338	337	341	343	348
							7.2				9.1		9.1		9.1				9.3					
-							551 1																435	468 ]
ഗ	v	ហ	ഗ	ഗ	Ξ	4	드	Ε	4	4	4	H	4	Ξ	Ξ	11	ω	G	4	13	Ξ	Ξ	4	
017760	062609	076259	061458	077069	070437	Q13485	P97471	054835	Q15798	Q15797	Q99717	P70340	014688	P70341	P97454	P70442	Q91913	P79947	015198	Q91693	035273	070520	014510	P97588
F01G10.8.	MATERNAL EFFECT ENHANC	MEDEA.	MEDEA.	MEDEA-B.	SMAD4 PROTEIN.	DPC4.	MAD HOMOLOG 4 (DELETIO	SMAD8.	SMAD5.	SMAD1.	MAD-LIKE PROTEIN.	MSMAD1.	SMAD5.	MSMAD5.	MAD HOMOLOG 1 (SMAD5).	MAD HOMOLOG 1 (MOTHERS	MAD1.	SMAD1.1.	MOTHER AGAINST DPP (MA	MOTHERS AGAINST DPP.	SMAD3.	SMAD1 PROTEIN.	SMAD 3.	MOTHERS AGAINST DPP 1
3.48e-1	4.30e-2	4.30e-2	4.30e-21	4.30e-2	1.87e-25	1.87e-2	1.25e-2	4.61e-34	1.28e-36	1.54e-3	1.54e-3	1.54e-37	6.60e-38	6.60e-3	.60e-	4.32e-3	1.54e-3	5.18e-3	3.38e-3	3.38e-3	5.18e-3	9.44e-4	4.03e-4	4.77e-4

## ALIGNMENTS

Ф	Оy	Оу	Од	Qy	Qy Db	Query Best Matcl	DR RA	R R R	R 0 0 0 0 1		RESULT ID O AC O
301 TETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLYAVYDQAVSIFYDL 360	241 LKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESPPPPYSRLSPRDEYKPLDLSDSTLSY 300 	181 KRLKERSLDTLLEAVESRGGVPGGCVLVPRADLRLGGQPAPPQLLLGRLFRWPDLQHAVE 240 	121 CETVTCCLFSERDAAGAPRDASDPLAGAALEPAGGGRSREARSRLLLLEQELKTVTYSLL 180 	61 RPVAPRRPRDAVGQRGAQGAGRRRRAGGPPRPMSEDGAGAGSSSLLDVAEPGGPGWLPESD 120, 	1 MFRSKRSGLVRRLWRSRVVPDREEGGSGGGGGGDEDGSLGSRAEPAPRAREGGGCGRSEV 60	Query Match 100.0%; Score 3630; DB 4; Length 496; Best Local Similarity 100.0%; Pred. No. 0.00e+00; Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	MOREN A.; SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS. EMBL; AF043640; G2828712; SEQUENCE 496 AA; 53497 MW; 310F8F08 CRC32;	SEQUENCE FROM N.A. TISSUE-PLACENTA;	SMAD6. HOMO SAPIENS (HUMAN). EUKARYOTA; METAAOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.	01-JUN-1998 (TREMBLREL. 06, CREATED) 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE) 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE) SMAD6.	LT 1 043654 PRELIMINARY; PRT; 496 AA. 043654;

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Best Local Similarity 99.8%;
Matches 495; Conservative
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O43541 PRELIMINARY;
O1-JUN-1998 (TREMBLREL 0
O1-JUN-1998 (TREMBLREL 0
O1-JUN-1998 (TREMBLREL 0
481
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HOMO SAPIENS (HUMAN).

""RARYOTA; METAZOA; CHORDATA;

"""NATNTDAE; HOMO.
                                             421
                                                          361
                                                                                                        301
                                                                                                                                                                                                                                                                                                           HATA A., LAGNA G., MASSAGUE J.
GENES DEV. 0:0-0(1997).
EMBL; AF035528; G2736516; -.
SEQUENCE 496 AA; 53496 MW;
                                                                           361
                                                                                           301
                                                                                                                        241
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                      IT_SCPCWLEILLNNPR 496
                                                              PQGSGFCLGQLNLEQRSESVRRTRSKIG5GILLSKEPDGVWAYNRGEHPIFVNSPTLDAP
                                                                                           TETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLYAVYDQAVSIFYDL
                                                                                                                                               CETVTCCLFSERDAAGAPRDASDPLAGAALEPAGGGRSREARSRLLLLEQELKTVTYSLL 180
                                                      PQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLSKEPDGVWAYNRGEHPIFVNSFTLDAP
                                                                                    TETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLYAVYDQAVSIFYDL
                                                                                                                 LKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESPPPPYSRLSPRDEYKPLDLSDSTLSY
                                                                                                                          LKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESDPPPYSRLSPRDEYKPLDLSDSTLSY
                                                                                                                                                                                                            RPVAPRRPRDAVGQRGAQGAGRRRRAGGPPRPMSEPGAGAGSSLLDVAEPGGPGWLPESD
                                                                                                                                                                                                                    RPVAPRRPRDAVGORGAGGAGRRRRAGGDPRPMSEPGAGAGSSLLDVAEPGGPGWLPESD
                                                                                                                                                                                                                                         ITSCPCWLEILLNNPR 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASSAGUE J.,
                                                                                                                                                                                                                                                                                                                                                                                      96,6
                                                                                                                                                                                                                                                                                   Score 3627; DB 4;
Pred. No. 0.00e+00;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

    Mismatches

                                                                                                                                                                                                                                                                                                                                                              VERTEBRATA;
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RESULT
ID Q1
AC Q1
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DT 01
DT 01
DT 01
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015799 015799; 01-NOV-1996 01-FEB-1997 01-NOV-1998

PRELIMINARY;

PRT;

235

(TREMBLREL. (TREMBLREL. (TREMBLREL.

802, 802,

CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)

SAPIENS

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RESULT 3
ID 035182;
AC 035182;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPD 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPD 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPD MAD HOWOLOG 7 (SMAD6).

GN MADH7 OR MSMAD6.
OC EVKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAM OC SCIUROGNATHI; MURIDAE; MURINAE; MUS.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97474881.
RA MIYAZONO K.;
RM MIYAZONO K.;
RT "Smad6 inhibits signalling by the TGF-beta sul NATURE 389:622-626(1997).
DR MGD: MGI:1100518; MADH7.
DR MGD; MGI:1100518; MADH7.
DR MGD; MGI:100518; MADH7.
DR PFAM; PFO0968; DWAFFIN; 1
SQ SEQUENCE 495 AA; 53714 MW; OCOB42D1 CRC32.
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Best Local
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EMBL; AF010133; G2507640; MGD; MGI:1100518; MADH7.
PFAM; PF00968; Dwarfin; 1.
SEQUENCE 495 AA; 53714 MW;
               478 QFITSCPCWLEILLNNHR 495
     479
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                                          DLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLSKEPDGVWAYNRGEHDIFVNSPTLD 419
                                                                                          DLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLSKEPDGVWAYNRGEHPIFVNSPTLD
                                                                                                                                         SYTETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLYAVYDQAVSIFY
                                                                                                                                                       SYTETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLYAVYDQAVSIFY 359
                                                                                                                                                                                                                                                                                           CETVTCCLFSERDAAGAPRDASDPLAGAALEPA-GGG-RSREARSRLLLLEQELKTVTYS
                                                                                                                                                                                                                                                                                                        CETVTCCLFSERDAAGAPRDSGDPQARQSPEPEEGGGPRSREARSRLLLLEQELKTVTYS
                                                                                                                                                                                                                                                                                                                                          h 92.3%;
Similarity 93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 3349; DB 11;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches 16;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 495;
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                                                                                                                                                                                                                                                                                                                                                              Query Match 41.5%;
Best Local Similarity 70.5%;
Matches 196; Conservative
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CATARRHINI;
[1]
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057475;
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SEQUENCE
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NAT. GENET. 13.347-449(1996).
EMBL; U59914; G164327: -.
PFAM; PF00968; Dwarfin; 1.
SEQUENCE 235 AA; 26235 MW; F69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HATA A., LAGNA G., MASSAGUE J., GENES DEV. 0:0-0(1997).
EMBL; AF035529; G2736318; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENOPUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIGGINS G.J., THIAGALINGAM S., HAMILTON S.R., WILLSON J.K., M VOGELSTEIN B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMAD6 (FRAGMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAYWEHRTRVGRLYAVYDQAVSIFYDLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILL
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  HGPPPHLLLCRLFRWPELQHPGQLKALSGCQGAGGSDNNSGCCCCCNPYHYSRVCEPESPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEPDGVWAYNRGEHPIFVNSPTLDAPGGRALVVRKVPPGYSIKVFDFERSGLQHAPEPD
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                                                                                                                 WEHRTRVGRLYAVCQPSVSIFYDLPQGSGFCLGQLNLENRSEAAARTRGKIGLGIVLSRE 180
                                                                                                                                                                                                        PPYSRLSPKIEQKPLDLSDS---YTEMEASNSLCITAADISDTSLSPDMSKQGHWCSVAY 120
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                                                                                                                                                                                  PPYSRLSPRDEYKPLDLSDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSVAY
                                                                                           WEHRTRVGRLYAVYDQAVSIFYDLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          31094 MW;
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Pred. No. 2.
45; Mismatc
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LAST SEQUENCE UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        685518EF CRC32;
                                                                                                                                                                                                                                                                                                                                                              re 1508; DB 13;
d. No. 2.00e-274;
Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEMMATI-BRIVANLOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280
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KINZLER K.
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Best Local Similarity 53.0%;
Matches 174; Conservative
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057459;
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057522;
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MAD-RELATED I
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SUBMITTED (FEB-1998) TO EMBL/GENBANK/DDBJ DATA
EMBL; AF026125; G3158344; -.
EMBL; AF045742; G3005093; -.
SEQUENCE 382 AA; 42713 MW; 22E7791D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAKAYAMA T., SNYDER M.A., GREWAL S.S., TS CHRISTIAN J.L.;
"Xenopus Smad8 acts downstream of BMP-4 t during vertebrate embryonic patterning.";
DEVELOPMENT 125:857-867(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XENOPODINAE; XENO
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|| ||| ||:|||:|||||||:::||
SFAKGWGPCYSRQFITSCPCWLEILLNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPTADSPDSVPSSTETGGTNFL--APEGLSDSQLLHETGDPSHWCMVAYWEEKTRVGRLY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADGPYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILL
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                                                                                                                                                                                                                              PRELIMINARY;
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Pred. No. 1.51e-234;
71; Mismatches 75;
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SMAD7.
XENOPUS LAEVIS (AFRICAN CLAWED FROG)
EUKARYOTA; METAZOA; CHORDATA; VERTEBI
MESOBATRACHIA; PIPOIDEA; PIPIDAE; XEI
[1]

VERTEBRATA; AMPHIBIA;

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088709;

01-NOV-1998 01
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
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CASELLAS R., HEMMATI-BRIVANLOU A.;
SUBMITIED (JAN-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF042198; G2921581; -.
SEQUENCE 382 AA; 42729 MW; 653E5184 CRC32;
                                                                                                                                                                                                      89
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                       PPPYSRY-PMDFLKPTGCPDAVPSSVETGGTNYL--APGGLSDSQLLLEPGDRSHWCVVA
                                                                                                                                              PPPYSRLSPRDEYKPLDLSDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSVA
                                                                                             PPSSYSLPLLLCKVFRWPDLRHSSEVKRLCCCESYGKI-NPELVCCNPHHLSRLCELESP 207
                                                                                           PP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVYDQAVSIFYDLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLSKEPDGVWAYNRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPL-DLSDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSVAYWEHRTRVGRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPTADSPDSVPSSTETGGTNEL--APEGLSDSQLLHETGDPSHWCMVAYWEEKTRVGRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFRWPDLQHAVELKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESPPPPYSRLSPRDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELKTVTYSLLKRLKERSLDTLLEAVESRGGVPGGCVLVPRADL--RLGGQPAPPQLLLGR
                                                                                                                                                                                                                                    l Similarity 53.8%;
183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (TREMBLREL. 08, )
3 (TREMBLREL. 08, )
3 (TREMBLREL. 08, )
D PROTEIN SMAD7B.
                                                                          *QLLLGRLFRWPDLQHAVELKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                       34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.6%;
                                                                                                                                                                                                                                    Score 1245; DB 11;
Pred. No. 3.92e-220;
65; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
70; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1293; DB 13;
Pred. No. 5.16e-230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425
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MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                 (Smad7
                                                                                                                                                                                                                                18;
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P SEQUENCE FROM N.A.

X MEDLINE; 97404392.

A TOPPER J.N., CAI J., QUI Y., ANDERSON K.R., XU Y.-Y., DEEDS A TOPPER J.N., CAI J., WOOLF E.A., TAYBER O., MAYS G.G., S SCHOEN F.J., GIMENO C.J., WOOLF E.A., TAYBER O., MAYS G.G., S SCHOEN F.J., GIMENO M.A. JR., FALB D.;

T "Vascular MADs: two novel MAD-related genes selectively included in human vascular endothelium."

PROC. NATL. ACAD. SCI. U.S.A. 94:9314-9319(1997).

R EMBL; AFO10193; G2252822; -

R PFAM; PF00966; Dwarfin; 1

SEQUENCE 426 AA; 46425 MW; 598F0022 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              015105;
015105;
01-JAN-1998
01-JAN-1998
01-NOV-1998
MAD-RELATED
            454
                                                  385
                                                                                        395
                                                                                                                            325
                                                                                                                                                                    335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAYASHI H., ABDOLLAH S., RICHARDSON M.A., TOPPER CELL 0:0-0(1997).
                                                                                                                                                                                                                                            276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                                                                                                        265
                                                                                                                                                                                                                                                                                  208
                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATARRHINI;
                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265
AADGPYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILLNN
                                                                          REVDGYWYINRSSYPIFIKSATLDNPDSRTLLVHKVFPGFSIKAFDYEKAYSLQRPNDHE
                                                                                                                                                    ATWEHRTRYGRIYAVYDQAVSIFYDLPQGSGFCLGQLNLEQRSESVRRTRSKIGFGILLS
                                                                                                                                                                                                                                                  PPPYSRY-PMDFLKPTADCPDAVPSSAETGGTNYL--APGGLSDSQLLLEPGDRSHWCVV 264
                                                                                                                                                                                                                                                                                                                                                                                                         EADLKALTHSVLKKLKERQLELLLQAVESRGGTRTACLLLPGRLDCRLGPGAPAGAQPAQ 148
                                                                                                                                                                            AYWEEKTRYGRLYCYQEPSLDIFYDLPQGNGFCLGQLNSDNKSQLYQKYRSKIGCGIQLT 324
                                                                                                                                                                                                                              PPPYSRLSPRDEYKPL-DLSDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSV
                                                                                                                                                                                                                                                                                                        PP----QLLLGRLFRWPDLQHAVELKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESP
                                                                                                                                                                                                                                                                                                                                PPSSYSLPLLLCKVFRWPDLRHSSEVKRLCCCESYGKI-NPELVCCNPHHLSRLCELESP 207
                                                                                                                                                                                                                                                                                                                                                                                     ADGPYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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8 (TREMBLREL.
9 GENE SMAD7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMINIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.N., GIMBRONE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1242; DB 4;
Pred. No. 1.62e-219;
66; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQ
LAST ANN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE UI
ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y.-Y., GRIN
JR., WRANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPDATE)
    494
                                        425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEDS J.D.,
.G., SAMPSON
                                                                          -GLQHAPEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
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FALB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMATES;
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                                                                          453
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RESULT 10 ID 014740

PRELIMINARY;

PRT;

426

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RESULT

AC OSS

AC OSS
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Best Local S
Matches 18
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O35253;

O1-JAN-1998 (TREMBLREL. (

O1-JAN-1998 (TREMBLREL. (

O1-NOV-1998 (TREMBLREL. (
                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 97474483.
NAKAO A., AFRAKHTE M., N
HEUCHEL R., ITOH S., KAN
TEN DIJKE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA;
CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q14740;
01-JAN-1998 (TREMBLREL.
01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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EMBL; AF01526; G26042; -.
PFAM; PF00968; Dwarfin; 1.
SEQUENCE 426 AA; 46471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAKAO A., AFRAKHTE M., MOREN A., NAKAYAMA T.,
HEUCHEL R., ITOH S., KAWABATA M., HELDIN N.E.,
TEN DIJKE P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 97474483.
                                                                                                                                                                                                                                                                                                                                                                                      MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                          signalling.";
NATURE 389:631-635(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAD HOMOLOG 8
MADH8 OR SMAD7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276
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                                    SEQUENCE FROM N.A.
                                                                                                                                         "Identification of Smad7, signalling.";
   FISSUE-WHOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
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les 184; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AADGPYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILLNN
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: | :|:|| | || || || ||:|||||||| ||:::|:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVDGYWYYNRSSYPIFIKSATLDNPDSRTLLVHKVFPGFSIKAFDYEKAYSLQRPNDHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYWEEKTRVGRLYCVQEPSLDIFYDLPQGNGFCLGQLNSDNKSQLVQKVRSKIGCGIQLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.2%;
larity 54.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 (SMAD7).
      EMBRYOS
                                                                                                                                                                                                                            ., MOREN A., NAKAYAMA T., CHRISTIAN KAWABATA M., HELDIN N.E., HELDIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05,
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                   TGFbeta-inducible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6462510B
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, HELDIN C.
                                                                                                                                                                antagonist of TGF-beta
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                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA;
                                                                                                                                                                                                                                   J.L.
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RESULT 12

RESULT 12

AC 088406;

AC 088406;

DT 01-NOV-1998;

DT 01-NOV-1998;

DT 01-NOV-1998;

DF SMAD7:

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Best Local Similarity 53.7%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KITAMURA K., OKAZAKI K.;

"Characterization of a novel mouse homologue of Mad, mediate TGF-beta family signalling.";

SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

EMBL; AF015260; G2460040; -.

EMBL; AJ000550; E1313653; -.

MGD; MGG:1100524; MADH8.

FFAM; PF00966; DWarfin; 1.

SEQUENCE 426 AA; 46441 MW; 61CE1D5B CRC32;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

CHEN Y., VALE W.;

"Inhibition of activin signaling by Smad7.";

SUBMITTED (JAN-1998) TO EMBL/GENBANK/DDBJ DA

EMBL; AF042499; G3282769;

SEQUENCE 425 AA; 46354 MW; F41D6DBB CRC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPYSRY-PMDFLKPTAGCPDAVPSSAETGGTNYL--APGGLSDSQLLLEPGDRSHWCVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQELKIVTYSLLKRLKERSLDTLLEAVESRGGVPGGCVLVP-RADLRLG-G----QPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EADLKALTHSVLKKLKERQLELLLQAVESRGGTRTACLLLLPGRLLDCRLGPGAPASAQPAQ 148
                                                                                                                                                                                                                  EADLKALTHSVLKKLKERQLELLLQAVESRGGTRTACLLLLPGRLDCRLGPGAPASAQPAQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FMQQPWTGFTVQISFVKGWGQCYTRQFISSCPCWLEVIFNS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPYSRLSPRDEYKPLDL-SDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSV
  PPPYSRLSPRDEYKPL-DLSDSTLSYTETEATNSLITAPGEFSDASMSPDATKPSHWCSV
                        PPPYSRY-PMDFLKPTADCPDAVPSSDETGGTNYL--APGGLSDSQLLLEPGDRSHWCVV
                                                                                              PP-----QLLLGRLFRWPDLQHAVELKPLCGCHSFAAAADGPTVCCNPYHFSRLCGPESP
                                                                                                                      PPSSYSLPLLLCKVFRWPDLRHSSEVKRLCCCESYGKI-N-PELVCNPHHLSRLCELESP 206
                                                                                                                                                                                         EQELKTVTYSLLKRLKERSLDTLLEAVESRGGVPGGCVLVP-RADLRLG-G-----QPA-
                                                                                                                                                                                                                                                                                       183;
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G (TREMBLREL.

G (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 6.72e-219;
66; Mismatches 73;
                                                                                                                                                                                                                                                                                     Score 1219; DB 11;
Pred. No. 8.70e-215;
66; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
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RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                               DATA
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                                                                                                                                                                                                                                                                                                                                 Length 425;
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AC QS
DT Q1
DT Q1
DT Q1
DT Q1
DT Q1
CREATER CORRESITE CORRESITATION C
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Best Local (
                                                                                                              Q91912;
Q91912;
Q1-NOV-1996
Q1-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Daughters against dpp modulates dy wing development."; NATURE 389:627-631(1997).
EMBL; AB004232; D1023711; -. PFAM; PF00968; Dwarfin; 1. SEQUENCE 568 AA; 63605 MW; B41
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYŪTA; METASOA; CHORDATA; VERTEBRATA; AMPHIBIA;
MESOBATRACHIA; PIPOIDEA; PIPIDAB; XENOPODINAE; XENOF
[1]
                                                                                 MAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O15968 PRELIMINARY;
O15968;
O1-JAN-1998 (TREMBLREL, O
01-JAN-1998 (TREMBLREL, O
01-NOV-1998 (TREMBLREL, O
DAD POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE;
                                                                                                                                                                                                                                                           444 SGLQHAPEPDA-ADGFYDPNSVRISFAKGWGPCYSRQFITSCPCWLEILLNNPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSE
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                  515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSUNEIZUMI K., NAKAYAMA T., CHRISTIAN J.L., TABATA T.;
                                                                                                                                                                                                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                                                                             458
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                                                                                                                                                                                                                                                                                           AELLSMRDHGHHPMGPVDYFSIKISFGKGWGRDYKRQDIMGCPCWLEVHFSHLR 568
                                                                                                                                                                                                                                                                                                                                      RSKIGFGILLSKEPDGVWAYNRGEHPIFVNSPTLDAPGGRALVVRKVPPGYSIKVFDFER
                                                                                                                                                                                                                                                                                                                                                             RHTVGLGVTLSLENGDVWIYNRGNTTIFVDSPTLSENLDR--VG-KVMPGVCLKAFETNR
                                                                                                                                                                                                                                                                                                                                                                                                                  H-WCSVAYWEHRTRYGRLYAVYDQAVSIFYD-L--PQGSGFCLGQLNLE-QRSESVRRT-
                                                                                                                                                                                                                                                                                                                                                                                                                                          QVWCQIAYWEMAHRVGEEFHAKTNAVNIYTDGIVASEVDSMCLRDLTPAGNQIHSVVPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQLLLGRLFRWPDLQHAVELKPLCGCHSFAAAADGPTVCCNPYH-FSRLCGPE--SPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REVDGVWVYNRSSYPIFIKSATLDNPDSRTLLVHKVFPGFSIKAFDYEKAYSLQRPNDHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPDGVWAYNRGEHPIFVNSPTLDAPGGRALVVRKVPPGYSIKVFDFERS-GLQHAPEPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113;
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                                                                                                          6 (TREMBLREL. 01, 06 (TREMBLREL. 01, 18 (TREMBLREL. 08, 1
                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.2%;
llarity 38.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                      , CREATED)
, LAST SEQUENCE UP
, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 515; DB 5;
Pred. No. 7.07e-73;
51; Mismatches 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAMOSHIDA Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 105;
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                                                                                                      UPDATE)
        XENOPUS
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                        BATRACHIA;
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20 밁 δÃ

389

334

RGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHDATVCKIPPGCNLKIFNNQEFAAL 393

WCSVAYWEHRTRYGRLYAVYDQAVSI--FYDLPQGSGFCLGQLNLEQRSESVRRTRSKIG

FGILLSKEPDGVWAYNRGEHPIFVNSPTLDAPGGR-ALVVRKVPPGYSIKVFDFER-SGL

446

388

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Best Local
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; T
ZHANG Y.-Q., KANZAKI M.,
"Rat Smad2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE; 96222291.

GRAFF J.M., BANSAL A., MELTON D.

"Xenopus Mad proteins transduce
TGF beta superfamily.";
CELL 85:479-487(1996).
EMBL, L77885; G1333645; ...

PFAM, PF00968; Dwarfin; 1.

SEQUENCE 467 AA; 52411 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ULT 15
O70436
PRI
070436
01-AUG-1998 (TI
01-AUG-1998 (TI
01-NOV-1998 (TI
SMAD2 PROTEIN.
                                                                                                                                                                                                                            SUBMITTED (SEP-1998) TO EMBL/GENBANK/DDBJ
EMBL; AF056001; G3025890; -
EMBL; AB017912; D1034419; -
SEQUENCE 467 AA; 52239 MW; FD9EFE07 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAMBA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OSAKI
                                274
                                                                         272
                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCIUROGNATHI; MURIDAE; MURINAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 LAQSVNQGFEAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGP
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WCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRHIG
                                                                             PETPPPGY--ISEDGETSDQOLNOSMDTGSPAELSPTTLS-PVNHS-LDLQPVTYSEPAF
                                                      PESPPPPYSRLSPRDEYKPLDLSDSTLSYTETEATNSLITAPGEFSDASMSPDA-TKPSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QHAPEPDAADGPYD-PN--SVRISFAKGWGPCYSRQFITSCPCWLEILLNNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WCSVAYWEHRTRVGRLYAVYDQAVSI--FYDLPQGSGFCLGQLNLEQRSESVRRTRSKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRRHIG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PETPPPGY--ISEDGETSDQOLNOSMDTGSPAELSPSTLS-PVN-HNLDLQPVTYSEPAF
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                                                                                                                                                   h 9.9%;
Similarity 32.3%;
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 10.0%;
Similarity 32.3%;
75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  YONEKURA A., MIYAZAKI Y., HIROTA Y., OHTSURU A., TSUKAZAKI T., SHINDO H., (MAR-1998) TO EMBL/GENBANK/DDBJ DATA
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3 (TREMBLREL.
6 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                      KANZAKI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07,
08,
                                                                                                                                            Score 361; DB 11;
Pred. No. 1.82e-43;
57; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 363; DB 13;
Pred. No. 7.73e-44;
57; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERTEBRATA;
E; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                               FD9EFE07 CRC32;
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                                                                                                                                                 88;
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YAMASHITA
BANKS.
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                                                                                                                                                                                                                                                                                             BANKS
                                                                                                                                                                                   Length 467;
                                                                                                                                          Indels
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Search completed: Fri Apr 30 20:39:41 1999 Job time : 104 secs.

